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Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val 35 40 45

Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln 50 55 60

Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu 65 70 75 80

Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr 85 90 95

Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp 100 105 110

Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn 115 120 125

Trp Glu Leu His Lys Glu Val Gly Thr Thr Pro Ile Val Thr Trp Leu 130 135 140

Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu 145 150 155 160

Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser 165 170 175

Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp 180 185 190

Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln 195 200 205

Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg 210 215 220

Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser 225 230 235 240

Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile 245 250 255

Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser 260 265 270

Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser 275 280 285

Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp 290 295 300

Tyr	Ser	Gln	Val	Arg	Asp	Ser	Ile	Gln	Ala	Tyr	Ser	Leu	Gly	Asp	Val
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Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met 325 330 335

Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met 340 345 350

Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser 355 360 365

His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu 370 375 380

Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile 385 390 395 400

Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe 405 410 415

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser 420 425 430

Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu 435 440 445

Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg 450 455 460

Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr 465 470 475 480

Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala 485 490 495

Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp 500 505 510

Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn 515 520 525

Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile

530 535 540

Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys 545 550 555 560

Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu 565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe 580 585

Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu 595 600

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu 625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser 645 650 655

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96

48

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	-							aac Asn 55			-					192
								gtg Val								240
								gtc Val								288
								tgg Trp								336
								gcc Ala								384
								cgc Arg 135								432
								cgg Arg								480
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								gat Asp								576
								cac His								624
								ctg Leu 215								672
			_	_		_	_	acg Thr		-						720
								aag Lys								768
ctc	gtg	gtt	gcc	ttc	ctg	gtc	tgc	tgg	gcc	cct	tac	cac	ttc	ttt	gcc	816

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gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe 290 295 300	912
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ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser 320 325 330	1008
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Ile	Asn	Gly 115	Val	Ile	Lys	Ala	Asn 120	Leu	Phe	Ile	Ser	Ile 125	Phe	Leu	Val
Val	Ala 130	Ile	Ser	Gln	Asp	Arg 135	Tyr	Arg	Val	Leu	Val 140	His	Pro	Met	Ala
Ser 145	Gly	Arg	Gln	Gln	Arg 150	Arg	Arg	Gln	Ala	Arg 155	Val	Thr	Cys	Val	Leu 160
Ile	Trp	Val	Val	Gly 165	Gly	Leu	Leu	Ser	Ile 170	Pro	Thr	Phe	Leu	Leu 175	Arg
Ser	Ile	Gln	Ala 180	Val	Pro	Asp	Leu	Asn 185	Ile	Thr	Ala	Cys	Ile 190	Leu	Leu
Leu	Pro	His 195	Glu	Ala	Trp	His	Phe 200	Ala	Arg	Ile	Val	Glu 205	Leu	Asn	Ile
Leu	Ģlу 210	Phe	Leu	Leu	Pro	Leu 215	Ala	Ala	Ile	Val	Phe 220	Phe	Asn	Tyr	His
Ile 225	Leu	Ala	Ser	Leu	Arg 230	Thr	Arg	Glu	Glu	Val 235	Ser	Arg	Thr	Arg	Val 240
Arg	Gly	Pro	Lys	Asp 245	Ser	Lys	Thr	Thr	Ala 250	Leu	Ile	Leu	Thr	Leu 255	Val
Val	Ala	Phe	Leu 260	Val	Cys	Trp	Ala		Tyr		Phe	Phe	Ala 270	Phe	Leu
Glu	Phe	Leu 275	Phe	Gln	Val	Gln	Ala 280	Val	Arg	Gly	Cys	Phe 285	Trp	Glu	Asp
Phe	Ile 290	Asp	Leu	Gly	Leu	Gln 295	Leu	Ala	Asn	Phe	Phe 300	Ala	Phe	Thr	Asn
Ser 305	Ser	Leu	Asn	Pro	Val 310	Ile	Tyr	Val	Phe	Val 315	Gly	Arg	Leu	Phe	Arg 320

Thr	Lys	Val	Trp	Glu	Leu	Tyr	Lys	Gln	Cys	Thr	Pro	Lys	Ser	Leu	Ala
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gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctc ctc tgc Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys 100 105 110	336
cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe 115 120 125	384
ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct Leu Val Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro	432

atg gcc agc gga agg cag cgg cgg agg cag gcc cgg gtc acc tgc Met Ala Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys qtq ctc atc tgq gtt gtq ggg ggc ctc ttg agc atc ccc aca ttc ctg Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr aga gtg cgg ggg ccg aag gat agc aag acc aca gcg ctg atc ctc acg Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cag ctc Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc Leu Ala Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe 

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Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala 130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 180 185 190

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		195					200					205			

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His 210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val 225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val 245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu 260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu Phe Arg 305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala 325 330 335

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Asn

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										aca Thr			144
	-									gtc Val	-		192
	_									atc Ile			240
										ttg Leu 90			288
				_						gga Gly	_		336
_	_			-		_	_			ttc Phe			384
										gtg Val			432
_	_									gcc Ala			480
										atc Ile 170			528
_	_			_	_		_	-		atc Ile			576
_					_				_	agg Arg		 	624
		_					_	_		atc Ile	-		672
			 -		_	_	_			gag Glu			720

Arg Val Arg Gly Pro Ly 240	ag gat agc aag ys Asp Ser Lys 245	acc aca gcg ctg a Thr Thr Ala Leu 1 250	atc ctc acg 768 Ile Leu Thr	
ctc gtg gtt gcc ttc ct Leu Val Val Ala Phe Le 255 26				
ttc ctg gaa ttc tta tt Phe Leu Glu Phe Leu Ph 275				
gag gac ttc att gac ct Glu Asp Phe Ile Asp Le 290		Leu Ala Asn Phe		
act aac agc tcc ctg aa Thr Asn Ser Ser Leu As 305				
ttc agg acc aag gtc to Phe Arg Thr Lys Val To 320				
ctt gct cca ata tct to Leu Ala Pro Ile Ser So 335				
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Ile	Trp	Asn	Gln 100	Phe	Asn	Trp	Pro	Phe 105	Gly	Ala	Leu	Leu	Cys 110	Arg	Val
Ile	Asn	Gly 115	Val	Ile	Lys	Ala	Asn 120	Leu	Phe	Ile	Ser	Ile 125	Phe	Leu	Val
Val	Ala 130	Ile	Ser	Gln	Asp	Arg 135	Tyr	Arg	Val	Leu	Val 140	His	Pro	Met	Ala
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Ile	Trp	Val	Val	Gly 165	Gly	Leu	Leu	Ser	Ile 170	Pro	Thr	Phe	Leu	Leu 175	Arg
Ser	Ile	Gln	Ala 180	Val	Pro	Asp	Leu	Asn 185	Ile	Thr	Ala	Cys	Ile 190	Leu	Leu
Leu	Pro	His 195	Glu	Ala	Trp	His	Phe 200	Ala	Arg	Ile	Val	Glu 205	Leu	Asn	Ile
Leu	Gly 210	Phe	Leu	Leu	Pro	Leu 215	Ala	Ala	Ile	Val	Phe 220	Phe	Asn	Tyr	His
Ile 225	Leu	Ala	Ser	Leu	Arg 230	Thr	Arg	Glu	Glu	Val 235	Ser	Arg	Thr	Arg	Val 240
Arg	Gly	Pro	Lys	Asp 245	Ser	Lys	Thr	Thr	Ala 250	Leu	Ile	Leu	Thr	Leu 255	Val

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu 260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 290 295 300

Ser Ser Leu 305	Asn Pro	Val Ile 310	Tyr Val	Phe Va 31		Arg Leu		Arg 320
Thr Lys Val	Trp Glu 325	Leu Tyr	Lys Gln	Cys Th	r Pro 1	Lys Ser	Leu <i>1</i> 335	Ala
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tgg gtg ctg Trp Val Leu 65					n Ile		Leu :	
gtc ttc tgc Val Phe Cys	-					-		
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aac Asn 225	atg Met	ctc Leu	ctg Leu	aat Asn	gtc Val 230	gtg Val	ggc Gly	ttc Phe	ctg Leu	ctg Leu 235	ccc Pro	ctg Leu	agt Ser	gtc Val	atc Ile 240	720
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Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr 115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val 195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr 210 215 220

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					gtc Val											522
					ttc Phe 110											570
					gtg Val											618
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Gly Asn Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg 50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser 65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn 85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro 100 105 110

Ile Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala 130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu 145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser 165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro 195 200 205 Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp 

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val 

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr 

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr 

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu 

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile 

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe 

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met 

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser 

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu 

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					gtg Val											1002
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Gly Asn Val Val Wat Trp Ile Ile Leu Ala His Lys Arg Met Arg 55

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser 75 70

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn 90

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro 100 105

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe 125 120 115

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala 140 135 130

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Cys Thr Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser 

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu 

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Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln

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gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc
Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Wet Trp Ile
45 50 55

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Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val

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Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val

75

80

85

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Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr

90 95 100

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Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro 195 200 205

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108

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Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu 370 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg 385 390 395 400

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Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu 435 440 445

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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser 225 230 235 240

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cageeteage t	ctcagttgc agccctg	yctg ctgcctgcct ggactt	gccc ctgccacctc 1660
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Asp Pro Glu 35		Arg Gly Glu Gly Lys Va 40 49	
Val Ile Ser 50	Lys Met Leu Phe `	Val Glu Pro Ile Leu G 60	lu Val Ser Ser
Leu Pro Thr 65	Thr Asn Ser Thr	Thr Asn Ser Ala Thr Ly 75	ys Ile Thr Ala 80
Asn Thr Thr	Asp Glu Pro Thr 85	Thr Gln Pro Thr Thr G	lu Pro Thr Thr 95
Gln Pro Thr	Ile Gln Pro Thr 100	Gln Pro Thr Thr Gln L 105	eu Pro Thr Asp 110
Ser Pro Thr		Gly Ser Phe Cys Pro G 120 1	ly Pro Val Thr 25

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp 130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Gly Met 145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn 260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp 290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn 340 345 350

Leu	Ser	Leu 355	Val	Ile	Leu	Val	Pro 360	Gln	Asn	Leu	Lys	His 365	Arg	Leu	Glu		
Asp	Met 370	Glu	Gln	Ala	Leu	Ser 375	Pro	Ser	Val	Phe	Lys 380	Ala	Ile	Met	Glu		
Lys 385		Glu	Met	Ser	Lys 390	Phe	Gln	Pro	Thr	Leu 395	Leu	Thr	Leu	Pro	Arg 400		
Ile	Lys	Val	Thr	Thr 405	Ser	Gln	Asp	Met	Leu 410	Ser	Ile	Met	Glu	Lys 415	Leu		
Glu	Phe	Phe	Asp 420	Phe	Ser	Tyr	Asp	Leu 425	Asn	Leu	Cys	Gly	Leu 430	Thr	Glu		
Asp	Pro	Asp 435	Leu	Gln	Val	Ser	Ala 440	Met	Gln	His	Gln	Thr 445	Val	Leu	Glu		
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Ala 465		Thr	Leu	Leu	Val 470	Phe	Glu	Val	Gln	Gln 475	Pro	Phe	Leu	Phe	Val 480		
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Me	. Ala	a Ser	Arg	Leu 5	Thr	Leu	Leu	ı Thr	Leu 10	Leu	. Lev	ı Leu	Leu	Lev 15	ı Ala		

156

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gtt Val	atc Ile 50	tcc Ser	aag Lys	atg Met	cta Leu	ttc Phe 55	gtt Val	gaa Glu	ccc Pro	atc Ile	ctg Leu 60	gag Glu	gtt Val	tcc Ser	agc Ser	252
ttg Leu 65	ccg Pro	aca Thr	acc Thr	aac Asn	tca Ser 70	aca Thr	acc Thr	aat Asn	tca Ser	gcc Ala 75	acc Thr	aaa Lys	ata Ile	aca Thr	gct Ala 80	300
aat Asn	acc Thr	act Thr	gat Asp	gaa Glu 85	ccc Pro	acc Thr	aca Thr	caa Gln	ccc Pro 90	acc Thr	aca Thr	gag Glu	ccc Pro	acc Thr 95	acc Thr	348
caa Gln	ccc Pro	acc Thr	atc Ile 100	caa Gln	ccc Pro	acc Thr	caa Gln	cca Pro 105	act Thr	acc Thr	cag Gln	ctc Leu	cca Pro 110	aca Thr	gat Asp	396
tct Ser	cct Pro	acc Thr 115	cag Gln	ccc Pro	act Thr	act Thr	ggg Gly 120	tcc Ser	ttc Phe	tgc Cys	cca Pro	gga Gly 125	cct Pro	gtt Val	act Thr	444
ctc Leu	tgc Cys 130	tct Ser	gac Asp	ttg Leu	gag Glu	agt Ser 135	cat His	tca Ser	aca Thr	gag Glu	gcc Ala 140	gtg Val	ttg Leu	GJÀ aaa	gat Asp	492
gct Ala 145	Leu	gta Val	gat Asp	ttc Phe	tcc Ser 150	ctg Leu	aag Lys	ctc Leu	tac Tyr	cac His 155	gcc Ala	ttc Phe	tca Ser	gca Ala	atg Met 160	540
aag Lys	aag Lys	gtg Val	gag Glu	acc Thr 165	aac Asn	atg Met	gcc Ala	ttt Phe	tcc Ser 170	cca Pro	ttc Phe	agc Ser	atc Ile	gcc Ala 175	agc Ser	588
ctc Leu	ctt Leu	Thr	cag Gln 180	Val	Leu	Leu	Gly	Ala	ggg	Gln	Asn	Thr	Lys	Thr	aac Asn	636
ctg Leu	gag Glu	ago Ser 195	Ile	ctc Leu	tct Ser	tac Tyr	ccc Pro 200	Lys	gac Asp	ttc Phe	acc Thr	tgt Cys 205	Val	cac His	cag Gln	684
gcc Ala	ctg Leu 210	Lys	ggc Gly	ttc Phe	acg Thr	acc Thr 215	Lys	ggt Gly	gtc Val	acc Thr	tca Ser 220	Val	tct Ser	cag Gln	atc Ile	732
ttc Phe 225	His	ago Ser	cca Pro	gac Asp	ctg Leu 230	Ala	ata Ile	agg Arg	gac Asp	acc Thr 235	Phe	gtg Val	aat Asn	gcc Ala	tct Ser 240	780
cgg Arg	acc Thr	ctg Lev	ı tacı ı Tyr	agc Ser	agc Ser	ago Ser	ccc	aga Arg	gto Val	cta Leu	agc Ser	aac Asn	aac Asn	agt Ser	gac Asp	828

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aag atc agc cgg Lys Ile Ser Arg 275	Leu Leu Asp S	agt ctg ccc Ser Leu Pro 280	tcc gat acc cgc Ser Asp Thr Arg 285	ctt gtc 924 Leu Val
ctc ctc aat gct Leu Leu Asn Ala 290	atc tac ctg a Ile Tyr Leu S 295	agt gcc aag Ser Ala Lys	tgg aag aca aca Trp Lys Thr Thr 300	ttt gat 972 Phe Asp
ccc aag aaa acc Pro Lys Lys Thr 305	aga atg gaa ( Arg Met Glu : 310	ccc ttt cac Pro Phe His	ttc aaa aac tca Phe Lys Asn Ser 315	gtt ata 1020 Val Ile 320
			cct gtg gcc cat Pro Val Ala His	
gac caa act ttg Asp Gln Thr Leu 340	Lys Ala Lys	gtg ggg cag Val Gly Gln 345	ctg cag ctc tcc Leu Gln Leu Ser 350	cac aat 1116 His Asn
ctg agt ttg gtg Leu Ser Leu Val 355	. Ile Leu Val	ccc cag aac Pro Gln Asn 360	ctg aaa cat cgt Leu Lys His Arg 365	Leu Glu
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			ctc cta aca cta Leu Leu Thr Leu 395	
atc aaa gtg acg Ile Lys Val Thr	g acc agc cag Thr Ser Gln 405	gat atg cto Asp Met Leu 410	c tca atc atg gag 1 Ser Ile Met Glu )	aaa ttg 1308 Lys Leu 415
gaa ttc ttc gat Glu Phe Phe Asr 420	Phe Ser Tyr	gac ctt aac Asp Leu Asr 425	c ctg tgt ggg ctg n Leu Cys Gly Leu 430	aca gag 1356 Thr Glu
gac cca gat ctt Asp Pro Asp Leu 435	cag gtt tct Gln Val Ser	gcg atg cag Ala Met Glr 440	g cac cag aca gtg n His Gln Thr Val 445	ctg gaa 1404 Leu Glu
ctg aca gag act Leu Thr Glu Thr 450	ggg gtg gag Gly Val Glu 455	gcg gct gca Ala Ala Ala	a gec tee gee ate a Ala Ser Ala Ile 460	Ser Val
gcc cgc acc cts Ala Arg Thr Lew 465	g ctg gtc ttt 1 Leu Val Phe 470	gaa gtg cag Glu Val Glr	g cag ccc ttc ctc n Gln Pro Phe Leu 475	ttc atg 1500 Phe Met 480

ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr 485 490 495	1548			
gac ccc agg gcc tgagacctgc aggatcaggt tagggcgagc gctacctctc Asp Pro Arg Ala 500	1600			
cagectcage teteagttge agecetgetg etgeetgeet ggaettgeee etgeeacete	1660			
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Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser 50 55 60				
Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala 65 70 75 80				
Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr 85 90 95				
Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp 100 105 110				
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr 115 120 125				

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp 130 135 140

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn 260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp 290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn 340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu

355 360	365
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Asp	Met 370	Glu	Gln	Ala	Leu	Ser 375	Pro	Ser	Val	Phe	380	Ala	lle	Met	GIU	
Lys 385	Leu	Glu	Met	Ser	Lys 390	Phe	Gln	Pro	Thr	Leu 395	Leu	Thr	Leu	Pro	Arg 400	
Ile	Lys	Val	Thr	Thr 405	Ser	Gln	Asp	Met	Leu 410	Ser	Ile	Met	Glu	Lys 415	Leu	
Glu	Phe	Phe	Asp 420	Phe	Ser	Tyr	Asp	Leu 425	Asn	Leu	Cys	Gly	Leu 430	Thr	Glu	
Asp	Pro	Asp 435	Leu	Gln	Val	Ser	Ala 440	Met	Gln	His	Gln	Thr 445	Val	Leu	Glu	
Leu	Thr 450		Thr	Gly	Val	Glu 455	Ala	Ala	Ala	Ala	Ser 460	Ala	Ile	Ser	Val	
Ala 465		Thr	Leu	Leu	Val 470	Phe	Glu	Val	Gln	Gln 475	Pro	Phe	Leu	Phe	Met 480	
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tcc Ser	cgg Arg	att Ile 25	gtg Val	gga Gly	ggc Gly	tgg Trp	gag Glu 30	tgt Cys	gag Glu	cag Gln	cat His	tcc Ser 35	cag Gln	ccc Pro	tgg Trp	150
cag Gln	gcg Ala 40	gct Ala	ctg Leu	tac Tyr	cat His	ttc Phe 45	agc Ser	act Thr	ttc Phe	cag Gln	tgt Cys 50	Gly ggg	ggc ggc	atc Ile	ctg Leu	198
gtg Val 55	cac His	cgc Arg	cag Gln	tgg Trp	gtg Val 60	ctc Leu	aca Thr	gct Ala	gct Ala	cat His 65	tgc Cys	atc Ile	agc Ser	gac Asp	aat Asn 70	246
tac Tyr	cag Gln	ctc Leu	tgg Trp	ctg Leu 75	ggt Gly	cgc Arg	cac His	aac Asn	ttg Leu 80	ttt Phe	gac Asp	gac Asp	gaa Glu	aac Asn 85	aca Thr	294
gcc Ala	cag Gln	ttt Phe	gtt Val 90	cat His	gtc Val	agt Ser	gag Glu	agc Ser 95	ttc Phe	cca Pro	cac His	cct Pro	ggc Gly 100	ttc Phe	aac Asn	342
					aac Asn											390
					ctc Leu											438
gat Asp 135	gct Ala	gtg Val	aag Lys	gtc Val	gtg Val 140	gag Glu	ttg Leu	ccc Pro	acc Thr	gag Glu 145	gaa Glu	ccc Pro	gaa Glu	gtg Val	ggg Gly 150	486
agc Ser	acc Thr	tgt Cys	ttg Leu	gct Ala 155	tcc Ser	ggc	tgg Trp	ggc Gly	agc Ser 160	atc Ile	gaa Glu	cca Pro	gag Glu	aat Asn 165	ttc Phe	534
					ctc Leu											582
gat Asp	gag Glu	tgc Cys 185	aaa Lys	aaa Lys	gcc Ala	cac His	gtc Val 190	cag Gln	aag Lys	gtg Val	aca Thr	gac Asp 195	ttc Phe	atg Met	ctg Leu	630
tgt Cys	gtc Val 200	gga Gly	cac His	ctg Leu	gaa Glu	ggt Gly 205	ggc	aaa Lys	gac Asp	acc Thr	tgt Cys 210	Val	ggt Gly	gat Asp	tca Ser	678
ggg Gly 215	Gly	ccg Pro	ctg Leu	atg Met	tgt Cys 220	gat Asp	ggt Gly	gtg Val	ctc Leu	caa Gln 225	Gly	gtc Val	aca Thr	tca Ser	tgg Trp 230	726
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gtg	ctg	tct	tat	gtg	aag	tgg	atc	gag	gac	acc	ata	gcg	gag	aac	tcc	822

Val Leu Ser Tyr Val Lys Trp Ile Glu Asp Thr Ile Ala Glu Asn Ser

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871

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<212> PRT

<213> homo sapiens

<400> 32

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Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
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Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe 35 40 45

Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala 50 55 60

His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu 65 70 75 80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe 85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu 115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr 130 135 140

Glu Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser 145  $\,$  150  $\,$  155  $\,$  160

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp 165 170 175

77-7 M1															
vai inr	Asp 195	Phe	Met	Leu	Cys	Val 200	Gly	His	Leu	Glu	Gly 205	Gly	Lys	Asp	
Thr Cys		Gly	Asp	Ser	Gly 215	Gly	Pro	Leu	Met	Cys 220	Asp	Gly	Val	Leu	
Gln Gly 225	· Val	Thr	Ser	Trp 230	Gly	Tyr	Val	Pro	Cys 235	Gly	Thr	Pro	Asn	Lys 240	
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tgc ctc	~~~								1				5		
Cys Leu									1 gct				att		102
tcc cgg Ser Arg	Ala att	Leu 10 gtg	Ser gga	Leu ggc	Gly tgg	Gly gag	Thr 15 tgt	Gly gag	1 gct Ala cag	Ala	Pro	Pro 20 cag	att Ile	Gln tgg	102 150
taa agg	att lle 25	Leu 10 gtg Val ctg	Ser gga Gly tac	Leu ggc Gly cat	Gly tgg Trp	Gly gag Glu 30 agc	Thr 15 tgt Cys	Gly gag Glu ttc	gct Ala cag Gln	Ala cat His	tcc Ser 35	Pro 20 cag Gln	att Ile ccc Pro	tgg Trp	
tcc cgg Ser Arg cag gcg Gln Ala	Ala att Ile 25 gct Ala	Leu 10 gtg Val ctg Leu	gga Gly tac Tyr	ggc Gly cat His	tgg Trp ttc Phe 45	gag Glu 30 agc Ser	Thr 15 tgt Cys act Thr	gag Glu ttc Phe	gct Ala cag Gln cag Gln	cat His tgt Cys 50	tcc Ser 35 ggg Gly	Pro 20 cag Gln ggc Gly	att Ile ccc Pro atc Ile	tgg Trp ctg Leu	150

Leu Lys Ile Leu Pro Asn Asp Glu Cys Lys Lys Ala His Val Gln Lys

185

gcc cag t Ala Gln P								42
atg agc c Met Ser L 1		-	_	-		-	_	90
cac gac c His Asp L 120								38
gat gct g Asp Ala V 135								86
agc acc t Ser Thr C		a Ser Gly						34
tca ttt c Ser Phe P		_						82
gat gag t Asp Glu C		-	-		_	_	_	30
tgt gtc g Cys Val G 200								78
ggg ggc c Gly Gly P 215								26
ggc tac g Gly Tyr V	_	s Gly Thr		_	_		-	74
gtg ctg t Val Leu S	_			_				22
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<213> homo sapiens

<400> 34

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			20					25					30		

- Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe 35 40 45
- Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala 50 60
- His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu 65 70 75 80
- Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe 85 90 95
- Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
  100 105 110
- Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
  115 120 125
- Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr 130 135 140
- Glu Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser 145 150 155 160
- Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp 165 170 175
- Leu Lys Ile Leu Pro Asn Asp Glu Cys Glu Lys Ala His Val Gln Lys 180 185 190
- Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp 195 200 205
- Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu 210 215 220
- Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys 225 230 235 240

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Thr Ile Ala Glu Asn Ser 260

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-		_	_		ctg Leu										102
					ggc Gly			_	-						150
_		_	_		cat His		_			_	_	 		_	198
		-	_		gtg Val 60			_	_		_		_		246
	_				ggt Gly										294
_	-		-		gtc Val										342
_	_		_		aac Asn					_	_	 _			390
					ctc Leu										438
_	_	_			gtg Val										486

135					140					145					150	
_	acc Thr	_	_	_					-		-					534
	ttt Phe		-	_			_		-							582
-	gag Glu	-			_		-	_	_	-						630
_	gtc Val 200			_												678
	ggc															726
	tac Tyr	_		_					_			_	-			774
	ctg Leu				_											822
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Gln	His	Ser 35	Gln	Pro	Trp	Gln	Ala 40	Ala	Leu	Tyr	His	Phe 45	Ser	Thr	Phe	
Gln	Cys 50	Gly	Gly	Ile	Leu	Val 55	His	Arg	Gln	Trp	Val 60	Leu	Thr	Ala	Ala	
His	Cys	Ile	Ser	Asp	Asn	Tyr	Gln	Leu	Trp	Leu	Gly	Arg	His	Asn	Leu	

Man And House

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe 85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
100 105 110

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ri,
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    <223> wherein N is either a "G" or an "A".
    <220>
    <221> misc_feature
    <222> (129)..(129)
    <223> wherein N is either a "T" or a "C".
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<220>

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<210> 290
<211> 353
<212> PRT
<213> homo sapiens
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<221> VARIANT
<222> (317)..(317)
<223> wherein Xaa is either "Arg" or "Gln".
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<221> VARIANT
<222>
      (241)..(241)
<223> wherein Xaa is either "Arg" or "Asn".
<220>
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<222>
      (191)..(191)
      wherein Xaa is either "Leu" or "Val".
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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
        35
                            40
Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
65
                    70
                                        75
Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
            100
                                105
                                                    110
Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
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140

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<221> misc\_feature

(543)..(543)

<223> wherein N is either a "T" or a "C".

<222>

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Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
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Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Xaa Leu
Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
    210
                        215
Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
                    230
Xaa Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
                                    250
                245
Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
            260
                                265
Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
        275
Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Xaa Leu Phe Arg
305
                    310
                                        315
                                                             320
Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
                325
                                    330
Pro Ile Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
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Asn
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Pro	Leu	Gln	Pro 140	Arg	Leu	Ser	Ala	Thr 145	Ala	Thr	Lys	Val	Val 150	Ile	Cys	
									gcc Ala							714
tca Ser	acc Thr 170	aca Thr	gag Glu	acc Thr	atg Met	ccc Pro 175	agc Ser	aga Arg	gtc Val	gtg Val	tgc Cys 180	atg Met	atc Ile	gaa Glu	tgg Trp	762
cca Pro 185	gag Glu	cat His	ccg Pro	aac Asn	aag Lys 190	att Ile	tat Tyr	gag Glu	aaa Lys	gtg Val 195	tac Tyr	cac His	atc Ile	tgt Cys	gtg Val 200	810
act Thr	gtg Val	ctg Leu	atc Ile	tac Tyr 205	ttc Phe	ctc Leu	ccc Pro	ctg Leu	ctg Leu 210	gtg Val	att Ile	ggc Gly	tat Tyr	gca Ala 215	tac Tyr	858
									agt Ser							906
tct Ser	gac Asp	cgc Arg 235	tac Tyr	cac His	gag Glu	caa Gln	gtc Val 240	tct Ser	gcc Ala	aag Lys	cgc Arg	aag Lys 245	gtg Val	gtc Val	aaa Lys	954
atg Met	atg Met 250	att Ile	gtc Val	gtg Val	gtg Val	tgc Cys 255	acc Thr	ttc Phe	gcc Ala	atc Ile	tgc Cys 260	tgg Trp	ctg Leu	ccc Pro	ttc Phe	1002
									aac Asn							1050
									atc Ile 290							1098
				Asn			Ile		tgc Cys		Leu	Asn		Arg		1146
									tgc Cys							1194
Gly	gac Asp 330	tat Tyr	gag Glu	Gly	ctg Leu	gaa Glu 335	atg Met	aaa Lys	tcc Ser	acc Thr	cgg Arg 340	tat Tyr	ctc Leu	cag Gln	acc Thr	1242
cag Gln 345	Gly	agt Ser	gtg Val	tac Tyr	aaa Lys 350	gtc Val	agc Ser	cgc Arg	ctg Leu	gag Glu 355	Thr	acc Thr	atc Ile	tcc Ser	aca Thr 360	1290
gtg Val	gtg Val	Gly	gcc Ala	cac His	gag Glu	gag Glu	gag Glu	cca Pro	gag Glu	gac Asp	ggc Gly	ccc Pro	aag Lys	gcc Ala	aca Thr	1338

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Marie Miller William William World Vandt Vandt

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Met Asp Asn Val Leu Pro Val Asp Ser Asp Leu Ser Pro Asn Ile Ser 1 10 15

Thr Asn Thr Ser Glu Pro Asn Gln Phe Val Gln Pro Ala Trp Gln Ile 20 25 30

Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val 35 40 45

Gly Asn Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg 50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser 65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn 85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Xaa Pro 100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala 130 135 140

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser 165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro 195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp 210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val 225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr 245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr 260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu

275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu 355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Xaa Ser Leu Asp Leu Thr Ser 370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser 385 390 395 400

Phe Ser Ser Asn Val Leu Ser 405

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<211> 1826

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<220>

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<222> (227)..(227)

<223> wherein N is either a "T" or a "C".

<220>

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<222> (536)..(536)

<223> wherein N is either a "C" or a "G".

<220>
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<222> (1498)..(1498)
<223> wherein N is either a "G" or an "A".

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<213> homo sapiens
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<221> VARIANT <222> (56)..(56)

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<220>

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<222> (159)..(159)

<223> wherein Xaa is either "Ala" or "Gly".

<220>

<221> VARIANT

<222> (480)..(480)

<223> wherein Xaa is either "Val" or "Met".

<400> 294

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Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Gln 20 25 30

Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr 35 40 45

Val Ile Ser Lys Met Leu Phe Xaa Glu Pro Ile Leu Glu Val Ser Ser 50 60

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385

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395

400

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg

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His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu 65 70 75 80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe 85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln 100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu 115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr

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Leu	. Lys	Ile	Leu 180	Pro	Asn	Asp	Glu	Cys 185	Xaa	Lys	Ala	His	Val 190	Gln	Lys	
Va]	Thr	Asp 195	Phe	Met	Leu	Cys	Val 200	Gly	His	Leu	Glu	Gly 205	Gly	Lys	Asp	
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Glr 225	_	· Val	Thr	Ser	Trp 230	Gly	Tyr	Val	Pro	Cys 235	Gly	Thr	Pro	Asn	Lys 240	
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<210> 556

<211> 353

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<213> Homo sapiens

<400> 556

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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala 20 25 30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val 115 120 Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala 135 140 Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg 170 Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 185 180 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile 200 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His 215 210 Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val 230 235 Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val 245 250 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu 265 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 285 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 295 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg 315 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala 330 Pro Ile Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg 345

Asn

<210> 557
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<222> (462)..(462)

## <223> wherein N is either a "G" or an "A".

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<210> 558 <211> 353 <212> PRT

<213> Homo sapiens

<400> 558

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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys

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Pro 65	Arg	Arg	Gln	Leu	Asn 70	Val	Ala	Glu	Ile	Tyr 75	Leu	Ala	Asn	Leu	Ala 80
Ala	Ser	Asp	Leu	Val 85	Phe	Val	Leu	Gly	Leu 90	Pro	Phe	Trp	Ala	Glu 95	Asn
Ile	Trp	Asn	Gln 100	Phe	Asn	Trp	Pro	Phe 105	Gly	Ala	Leu	Leu	Cys 110	Arg	Val
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Leu	Gly 210	Phe	Leu	Leu	Pro	Leu 215	Ala	Ala	Ile	Val	Phe 220	Phe	Asn	Tyr	His
Ile 225	Leu	Ala	Ser	Leu	Arg 230	Thr	Arg	Glu	Glu	Val 235	Ser	Arg	Thr	Arg	Val 240
Arg	Gly	Pro	Lys	Asp 245	Ser	Lys	Thr	Thr	Ala 250	Leu	Ile	Leu	Thr	Leu 255	Val
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Glu	Phe	Leu 275	Phe	Gln	Val	Gln	Ala 280	Val	Arg	Gly	Cys	Phe 285	Trp	Glu	Asp
Phe	Ile 290	Asp	Leu	Gly	Leu	Gln 295	Leu	Ala	Asn	Phe	Phe 300	Ala	Phe	Thr	Asn
Ser 305	Ser	Leu	Asn	Pro	Val 310	Ile	Tyr	Val	Phe	Val 315	Gly	Arg	Leu	Phe	Arg 320
Thr	Lys	Val	Trp	Glu 325	Leu	Tyr	Lys	Gln	Cys 330	Thr	Pro	Lys	Ser	Leu 335	Ala

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Asn

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<210> 559
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<222> (577)..(577)
<223> wherein N is either a "C" or a "G".
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- <211> 353 <212> PRT <213> Homo sapiens <220> <221> VARIANT <222> (191)..(191) <223> wherein Xaa is either "Leu" or "Val". <400> 560 Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser 55 85
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Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 290 295 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg 310 315 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala 325 330 335 Pro Ile Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg 340 345 Asn <210> 561 <211> 1082 <212> DNA <213> Homo sapiens

<220>

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<222> (705)..(705)

<223> wherein N is either a "G" or an "A".

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<211> 353

<212> PRT

<213> Homo sapiens

<400> 562

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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala 20 25 30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu 50 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala 130 135 140

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg  $165 \hspace{1.5cm} 170 \hspace{1.5cm} 175 \hspace{1.5cm}$ 

Leu	Pro	His 195	Glu	Ala	Trp	His	Phe 200	Ala	Arg	Ile	Val	Glu 205	Leu	Asn	Ile	
Leu	Gly 210	Phe	Leu	Leu	Pro	Leu 215	Ala	Ala	Ile	Val	Phe 220	Phe	Asn	Tyr	His	
Ile 225	Leu	Ala	Ser	Leu	Arg 230	Thr	Arg	Lys	Glu	Val 235	Ser	Arg	Thr	Arg	Val 240	
Arg	Gly	Pro	Lys	Asp 245	Ser	Lys	Thr	Thr	Ala 250	Leu	Ile	Leu	Thr	Leu 255	Val	
Val	Ala	Phe	Leu 260	Val	Cys	Trp	Ala	Pro 265	Tyr	His	Phe	Phe	Ala 270	Phe	Leu	
Glu	Phe	Leu 275	Phe	Gln	Val	Gln	Ala 280	Val	Arg	Gly	Cys	Phe 285	Trp	Glu	Asp	
Phe	Ile 290	Asp	Leu	Gly	Leu	Gln 295	Leu	Ala	Asn	Phe	Phe 300	Ala	Phe	Thr	Asn	
Ser 305	Ser	Leu	Asn	Pro	Val 310	Ile	Tyr	Val	Phe	Val 315	Gly	Arg	Leu	Phe	Arg 320	
Thr	Lys	Val	Trp	Glu 325	Leu	Tyr	Lys	Gln	Cys 330	Thr	Pro	Lys	Ser	Leu 335	Ala	
Pro	Ile	Ser	Ser 340	Ser	His	Arg	Lys	Glu 345	Ile	Phe	Gln	Leu	Phe 350	Trp	Arg	
Asn																
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<220 <221 <222 <223	L> r 2>	misc (40) where	(40	))	eitl	ner a	a "C'	' or	a "[	Γ".						
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acct	ttg	ada a	agago	caaat	tg co	cccc	agto	g gag	gtggd	ctgg	gate	ggcto	caa (	cacca	atccag	180
ccc	ccctt	ccc t	ctgg	ggtgd	ct gt	tcgt	gatg	g gco	cacco	ctag	agaa	acato	ctt t	tgtco	ctcagc	240

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 180 185 190

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3733

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Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe  $100 \hspace{1cm} 105 \hspace{1cm} 110$ 

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val 195 200 205

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Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro 35 40 45

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr 115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val 195 200 ^ 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr 210 215 220

Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile 225 230 235 240

Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met

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360

420

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<213> Homo sapiens

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<223> wherein Xaa is either "Gly" or "Glu".

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Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr 115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val 145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Ser Ser Pro Met 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val 195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr 210 215 220

Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile 225 230 235 240

Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met 245 250 255

Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val 260 265 270	
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- Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln 85 90 95
- Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys 100 105 110
- Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser 115 120 125
- Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu 130 135 140
- Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu 145 150 155 160
- Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu 165 170 175
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- Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu 210 215 220
- Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu 225 230 235 240
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- Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly 260 265 270
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- Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro 325 330 335
- Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly 340 345 350
- Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp 355 360 365
- Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala 370 375 380

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680

685

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<213> Homo sapiens

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Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser 20 25 30

Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser 35 40 45

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr 50 55 60

Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu 70 75 80

Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His 85 90 95

Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu 100 105 110

Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu 115 120 125

Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe 130 135 140

Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met 145 150 155 160

Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val 165 170 175

- Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
  180 185 190
- Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val 195 200 205
- Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile 210 215 220
- Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr 225 230 235 240
- Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu 245 250 255
- His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
  260 265 270
- Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu 275 280 285
- Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu 290 295 300
- Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys 305 310 315 320
- Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu 325 330 335
- Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr 340 345 350
- Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu 355 360 365
- Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala 370 375 380 .
- Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn 385 390 395 400
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- <221> misc\_feature
- <222> (699)..(699)

<223> wherein N is either a "C" or a "T".

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cggcccttcc	ttgtggtgat	cttttccacc	agcacccaga	gtgtcctctt	tctgggcaag	1260
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Met His Leu Ile Asp Tyr Leu Leu Leu Leu Val Gly Leu Leu Ala

<sup>&</sup>lt;210> 574 <211> 427 <212> PRT <213> Homo sapiens

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Leu 65	Ile	Ala	Ser	Glu	Thr 70	Pro	Gly	Lys	Asn	Ile 75	Phe	Phe	Ser	Pro	Leu 80
Ser	Ile	Ser	Ala	Ala 85	Tyr	Ala	Met	Leu	Ser 90	Leu	Gly	Ala	Cys	Ser 95	His
Ser	Arg	Ser	Gln 100	Ile	Leu	Glu	Gly	Leu 105	Gly	Phe	Asn	Leu	Thr 110	Glu	Leu
Ser	Glu	Ser 115	Asp	Val	His	Arg	Gly 120	Phe	Gln	His	Leu	Leu 125	His	Thr	Leu
Asn	Leu 130	Pro	Gly	His	Gly	Leu 135	Glu	Thr	Arg	Val	Gly 140	Ser	Ala	Leu	Phe
Leu 145	Ser	His	Asn	Leu	Lys 150	Phe	Leu	Ala	Lys	Phe 155	Leu	Asn	Asp	Thr	Met 160
Ala	Val	Tyr	Glu	Ala 165	Lys	Leu	Phe	His	Thr 170	Asn	Phe	Tyr	Asp	Thr 175	Val
Gly	Thr	Ile	Gln 180	Leu	Ile	Asn	Asp	His 185	Val	Lys	Lys	Glu	Thr 190	Arg	Gly
Lys	Ile	Val 195	Asp	Leu	Val	Ser	Glu 200	Leu	Lys	Lys	Asp	Val 205	Leu	Met	Val
Leu	Val 210	Asn	Tyr	Ile	Tyr	Phe 215	Lys	Ala	Leu	Trp	Glu 220	Lys	Pro	Phe	Ile
Ser	Ser	Ara	Thr	Thr	Pro	Lvs	Asp	Phe	Tvr	Val	Asp	G111	Asn	Thr	Thr

Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu 245 250 255

230

His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly 260 265 270

Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu 275 280 285

Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu 290 295 300

Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys

235

240

305	310	315	320
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Gly Phe Thr Asp Leu 340	Phe Ser Lys Trp Ala 345	Asp Leu Ser Gly Ile 350	Thr
Lys Gln Gln Lys Leu 355	Glu Ala Ser Lys Ser 360	Phe His Lys Ala Thr 365	Leu
Asp Val Asp Glu Ala 370	Gly Thr Glu Ala Ala 375	Ala Ala Thr Thr Phe 380	Ala
Ile Lys Phe Phe Ser 385	Ala Gln Thr Asn Arg 390	His Ile Leu Arg Phe 395	Asn 400
Arg Pro Phe Leu Val 405	Val Ile Phe Ser Thr 410	Ser Thr Gln Ser Val 415	Leu
Phe Leu Gly Lys Val 420	Val Asp Pro Thr Lys 425	Pro	
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60 120 180 gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 240 cgcttctact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctccccgctg agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300 atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360 420 ttccagcacc tcctgcacac tctcaacctc cccggccatg ggctggaaac acgcgtgggc 480 agtgctctgt tcctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg gccgtctatg aggctaaact cttccacacc aacttctacg acactgtggg cacaatccag 540 cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagcgag 600 ctcaagaagg acgtcttgat ggtgctggtg aattacattt acttcaaagc cctgtgggag 660

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Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser 35 40 45

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr 50 55 60

Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu 65 70 75 80

Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His 85 90 95

Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu 100 105 110

Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu 115 120 125

Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe 130 135 140

Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met 145 150 155 160

Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val 165 170 175

Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly 180 185 190

Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val 195 200 205

Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile 210 215 220

Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr 225 230 235 240

Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu 245 250 255

His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly 260 265 270

Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu 275 280 285

Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu 290 295 300

Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys 305 310 315 320

Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu 325 330 335

Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr 340 345 350

Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu 355 360 365

Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala 370 375 380

Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn 395 400

Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu 405 410 415

Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro 420 425

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<223> wherein N is either a "C" or a "G".
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<223> wherein N is either a "T" or a "C".
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gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc
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egettetact acetgatege tteggagace eeggggaaga acatetttt eteceegetg
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<222> (138)..(138)

<223> wherein Xaa is either "Arg" or a "Cys".

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Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser 35 40 45

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr 50 55 60

Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu 65 70 75 80

Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His 85 90 95

Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu 100 105 110

Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu 115 120 125

Asn Leu Pro Gly His Gly Leu Glu Thr Xaa Val Gly Ser Ala Leu Phe 130 135 140

Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met 145 150 150 155

- Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val 165 170 175
- Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
  180 185 190
- Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val 195 200 205
- Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile 210 215 220
- Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr 225 230 235 240
- Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
  245 250 255
- His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly 260 265 270
- Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu 275 280 285
- Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu 290 295 300
- Leu Arg Lys Arg Asn Phe Tyr Lys Leu Glu Leu His Leu Pro Lys 305 310 315 320
- Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu 325 330 335
- Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr 340 345 350
- Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu 355 360 365
- Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala 370 375 380
- Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn 385 390 395 400
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il a f	<210>	583
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	Ile	Trp	Asn	Gln 100	Phe	Asn	Trp	Pro	Phe 105	Gly	Ala	Leu	Leu	Cys 110	Arg	Val	
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165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile 195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His 210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val 225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val 245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu 260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg 305 310 315 320

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Pro Ile Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg 340 345 350

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<213> Oryctolagus cuniculus

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Leu Gly Leu Leu Gly Asn Ser Phe Val Leu Ser Val Phe Leu Leu Ala 50 55 60

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Ser	Asp	Leu	Val	Phe 85	Val	Leu	Gly	Leu	Pro 90	Phe	Trp	Ala	Glu	Asn 95	Val
Arg	Asn	Gln	Phe 100	Asp	Trp	Pro	Phe	Gly 105	Ala	Ala	Leu	Cys	Arg 110	Ile	Val
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Ala	Ile 130	Ser	Gln	Asp	Arg	Tyr 135	Ser	Val	Leu	Val	His 140	Pro	Met	Ala	Ser
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Trp	Leu	Ala	Gly	Gly 165	Leu	Leu	Ser	Thr	Pro 170	Thr	Phe	Val	Leu	Arg 175	Ser
Val	Arg	Ala	Val 180	Pro	Glu	Leu	Asn	Val 185	Ser	Ala	Cys	Iļe	Leu 190	Leu	Leu
Pro	His	Glu 195		Trp	His	Trp	Leu 200	Arg	Met	Val	Glu	Leu 205	Asn	Leu	Leu
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Gly	Pro	Arg	Asp	Ser 245	Lys	Ser	Thr	Ala	Leu 250		Leu	Thr	Leu	Val 255	Ala
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Cys	Leu	Trp 275		. Val	. His	Ala	11e 280		Gly	Cys	Phe	285	Glu	Glu	. Phe
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Cys Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg Thr 305 310 315 320

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Val Ser Ser Ser Arg Arg Lys Glu Met Leu Trp Gly Phe Trp Arg Asn 340 345 350

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<211> 337

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<400> 837

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20 25 30

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Phe Gly Leu Leu Gly Asn Leu Leu Val Leu Ser Phe Phe Leu Leu Pro 50 55 60

Trp Arg Gln Trp Trp Gln Gln Arg Gln Arg Gln Gln Arg Leu Thr 65 70 75 80

Ile Ala Glu Ile Tyr Leu Ala Asn Leu Ala Ala Ser Asp Leu Val Phe 85 90 95

Val Leu Gly Leu Pro Phe Trp Ala Glu Asn Ile Gly Asn Arg Phe Asn 100 105 110

Trp Pro Phe Gly Thr Asp Leu Cys Arg Val Val Ser Gly Val Ile Lys
115 120 125

Ala Asn Leu Phe Val Ser Ile Phe Leu Val Val Ala Ile Ser Gln Asp 130 135 140

Arg Tyr Arg Leu Leu Val Tyr Pro Met Thr Ser Trp Gly Tyr Arg Arg 145 150 155 160

Arg Arg Gln Ala Gln Ala Thr Cys Leu Leu Ile Trp Val Ala Gly Gly
165 170 175

Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg Ser Val Lys Val Val Pro 180 185 190

Asp Leu Asn Val Ser Ala Cys Ile Leu Leu Phe Pro His Glu Ala Trp 195 200 205

His Phe Ala Arg Met Val Glu Leu Asn Val Leu Gly Phe Leu Leu Pro 210 215 220

Val Thr Ala Ile Ile Phe Phe Asn Tyr His Ile Leu Ala Ser Leu Arg 225 230 235 240

Gly Gln Lys Glu Ala Ser Arg Thr Arg Cys Gly Gly Pro Lys Gly Ser 245 250 255

Lys Thr Thr Gly Leu Ile Leu Thr Leu Val Ala Ser Phe Leu Val Cys 260 265 270

Trp Cys Pro Tyr His Phe Phe Ala Phe Leu Asp Phe Leu Val Gln Val 275 280 285 Arg Val Ile Gln Asp Cys Ser Trp Lys Glu Ile Thr Asp Leu Gly Leu 290 295 300

Gln Leu Ala Asn Phe Phe Ala Phe Val Asn Ser Cys Leu Asn Pro Leu 305 310 315 320

Ile Tyr Val Phe Ala Gly Arg Leu Leu Lys Thr Arg Val Leu Gly Thr 325 330 335

Leu

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Gln Val Leu Gly Ser Ala Leu Asn Gly Thr Leu Ser Lys Asp Asn Cys 35 40 45

Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile Gln Ala Pro Phe 50 55 60

Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn Leu Phe Val Leu 65 70 75 80

Ser Val Phe Phe Leu His Lys Asn Ser Cys Thr Val Ala Glu Ile Tyr 85 90 95

Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro
100 105 110

Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp Val Phe Gly Glu
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Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met Asn Leu Tyr Ser 130 135 140

Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu 145 150 155 160

Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys 165 170 175

Leu Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro 180 185 190

Met Leu Val Phe Arg Thr Met Arg Glu Tyr Ser Glu Glu Gly His Asn

195	200	205

Val Thr Ala Cys Val Ile Val Tyr Pro Ser Arg Ser Trp Glu Val Phe 210 215 220

Thr Asn Val Leu Leu Asn Leu Val Gly Phe Leu Leu Pro Leu Ser Val 225 230 235 240

Ile Thr Phe Cys Thr Val Arg Ile Leu Gln Val Leu Arg Asn Asn Glu 245 250 255

Met Lys Lys Phe Lys Glu Val Gln Thr Glu Arg Lys Ala Thr Val Leu 260 265 270

Val Leu Ala Val Leu Gly Leu Phe Val Leu Cys Trp Val Pro Phe Gln 275 280 285

Ile Ser Thr Phe Leu Asp Thr Leu Leu Arg Leu Gly Val Leu Ser Gly 290 295 300

Cys Trp Asp Glu His Ala Val Asp Val Ile Thr Gln Ile Ser Ser Tyr 305 310 315 320

Val Ala Tyr Ser Asn Ser Gly Leu Asn Pro Leu Val Tyr Val Ile Val 325 330 335

Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr Arg Val Leu Cys 340 345 350

Gln Lys Gly Gly Cys Met Gly Glu Pro Val Gln Met Glu Asn Ser Met 355 360 365

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Gln Asp Trp Ala Gly Lys Lys Gln 385 390

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<213> Oryctolagus cuniculus

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Asn Val Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Val Leu Ala Thr 35 40 45

Leu Glu Asn Leu Phe Val Leu Ser Val Phe Cys Leu His Lys Ser Ser 50 55 60

- Cys Thr Val Ala Glu Val Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu 65 70 75 80
- Ile Leu Ala Cys Gly Leu Pro Phe Trp Ala Val Thr Ile Ala Asn His 85 90 95
- Phe Asp Trp Leu Phe Gly Glu Ala Leu Cys Arg Val Val Asn Thr Met 100 105 110
- Ile Tyr Met Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser 115 120 125
- Ile Asp Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Ile Gly Arg Met 130 135 140
- Arg Arg Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys 145 150 155 160
- Thr Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp 165 170 175
- Tyr Arg Asp Glu Gly Tyr Asn Val Thr Ala Cys Ile Ile Asp Tyr Pro 180 185 190
- Ser Arg Ser Trp Glu Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly
  195 200 205
- Phe Leu Leu Pro Leu Ser Val Ile Thr Phe Cys Thr Val Gln Ile Leu 210 215 220
- Gln Val Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr 225 230 235 240
- Glu Arg Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Leu Phe Val 245 250 255
- Val Cys Trp Leu Pro Phe Gln Val Ser Thr Phe Leu Asp Thr Leu Leu 260 265 270
- Lys Leu Gly Val Leu Ser Ser Cys Trp Asp Glu His Val Ile Asp Val 275 280 285
- Ile Thr Gln Val Gly Ser Phe Met Gly Tyr Ser Asn Ser Cys Leu Asn 290 295 300
- Pro Leu Val Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg 305 310 315 320
- Glu Val Tyr Arg Ala Ala Cys Pro Lys Ala Gly Cys Val Leu Glu Pro 325 330 335
- Val Gln Ala Glu Ser Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val
- Glu Arg Gln Ile His Lys Leu Pro Glu Trp Thr Arg Ser Ser Gln 355 360 365

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<211> 372

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Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Val Leu Ala Val Leu Glu 35 40 45

Asn Ile Phe Val Leu Ser Val Phe Phe Leu His Lys Ser Ser Cys Thr 50 55 60

Val Ala Glu Ile Tyr Leu Gly Asn Leu Ala Val Ala Asp Leu Ile Leu 65 70 75 80

Ala Phe Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp 85 90 95

Trp Leu Phe Gly Glu Val Leu Cys Arg Met Val Asn Thr Met Ile Gln 100 105 110

Met Asn Met Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp 115 120 125

Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Met Gly Arg Met Arg Gly
130 140

Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys Ala Leu 145 150 155 160

Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp Tyr Arg 165 170 175

Asp Glu Gly His Asn Val Thr Ala Cys Leu Ile Ile Tyr Pro Ser Leu 180 185 190

Thr Trp Gln Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly Phe Leu 195 200 205

Leu Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Gln Ile Met Gln Val 210 215 220

Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg 225 230 235 240

Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Leu Phe Val Val Cys 245 250 255

Trp Leu Pro Phe Gln Ile Gly Thr Phe Leu Asp Thr Leu Arg Leu Leu 260 265 270

Gly Phe Leu Pro Gly Cys Trp Glu His Val Ile Asp Leu Ile Thr Gln 275 280 285

Ile Ser Ser Tyr Leu Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val 290 295 300

Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr 305 310 315 320

His Gly Leu Cys Arg Ser Gly Gly Cys Val Ser Glu Pro Ala Gln Ser 325 330 335

Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln 340 345 350

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<211> 396

<212> PRT

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<400> 841

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Val Phe Trp Gly Pro Gly Cys His Leu Ser Thr Cys Ile Glu Met Phe 20 25 30

Asn Ile Thr Thr Gln Ala Leu Gly Ser Ala His Asn Gly Thr Phe Ser 35 40 45

Glu Val Asn Cys Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile 50 60

Gln Ala Pro Phe Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn 65 70 75 80

Ile Phe Val Leu Ser Val Phe Cys Leu His Lys Thr Asn Cys Thr Val 85 90 95

Ala Glu Ile Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala 100 105 110

Cys Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp 115 120 125

Leu Phe Gly Glu Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met 130 135 140

Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg

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165

Tyr Leu Ala Leu Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val 170

Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Ser Cys Thr Leu Leu 180

Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp Tyr Arg Glu 200

Glu Gly His Asn Val Thr Ala Cys Val Ile Val Tyr Pro Ser Arg Ser 215

Trp Glu Val Phe Thr Asn Met Leu Leu Asn Leu Val Gly Phe Leu Leu 235 230

Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Arg Ile Met Gln Val Leu 250

Arg Asn Asn Glu Met Lys Lys Phe Lys Glu Val Gln Thr Glu Lys Lys 265

Ala Thr Val Leu Val Leu Ala Val Leu Gly Leu Phe Val Leu Cys Trp 285

Phe Pro Phe Gln Ile Ser Thr Phe Leu Asp Thr Leu Leu Arg Leu Gly 300

Val Leu Ser Gly Cys Trp Asn Glu Arg Ala Val Asp Ile Val Thr Gln 315

Ile Ser Ser Tyr Val Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val 330

Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr 345

Gln Ala Ile Cys Arg Lys Gly Gly Cys Met Gly Glu Ser Val Gln Met 360

Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln 375

Ile His Lys Leu Gln Asp Trp Ala Gly Asn Lys Gln 390 385

<210> 842

<211> 3405

DNA <212>

<213> homo sapiens

<220>

<221> misc\_feature

(2173)..(2173) <222>

<223> wherein N is either a "T" or a "C".

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1740 agaagcactt tgtcaagcag ctaaacatga aggccctctg cacaaatgtg acatctcaaa 1800 ctctacagaa gctggacaga aactgttcaa tatgctgagg cttggaaaat cagaaccctg 1860 gaccctagca ttggaaaatg ttgtaggagc aaagaacatg aatgtaaggc cactgctcaa 1920 ctactttgag cccttattta cctggctgaa agaccagaac aagaattctt ttgtgggatg 1980 gagtaccgac tggagtccat atgcagacca aagcatcaaa gtgaggataa gcctaaaatc agctcttgga gataaagcat atgaatggaa cgacaatgaa atgtacctgt tccgatcatc 2040 tgttgcatat gctatgaggc agtacttttt aaaagtaaaa aatcagatga ttctttttgg 2100 ggaggaggat gtgcgagtgg ctaatttgaa accaagaatc tcctttaatt tctttgtcac 2160 2220 tgcacctaaa aacgtgtctg atatcattcc tagaactgaa gttgaaaagg ccatcaggat 2280 gtcccggagc cgtatcaatg atgctttccg tctgaatgac aacagcctag agtttctggg 2340 gatacagcca acacttggac ctcctaacca gccccctgtt tccatatggc tgattgtttt tggagttgtg atgggagtga tagtggttgg cattgtcatc ctgatcttca ctgggatcag 2400 2460 agatcggaag aagaaaaata aagcaagaag tggagaaaat ccttatgcct ccatcgatat tagcaaagga gaaaataatc caggattcca aaacactgat gatgttcaga cctcctttta 2520 2580 gaaaaatcta tgtttttcct cttgaggtga ttttgttgta tgtaaatgtt aatttcatgg 2640 tatagaaaat ataagatgat aaagatatca ttaaatgtca aaactatgac tctgttcaga 2700 aaaaaaattg tccaaagaca acatggccaa ggagagagca tcttcattga cattgctttc agtatttatt totgtototg gatttgactt otgttotgtt tottaataag gattttgtat 2760 2820 tagagtatat tagggaaagt gtgtatttgg tctcacaggc tgttcaggga taatctaaat 2880 gtaaatgtct gttgaatttc tgaagttgaa aacaaggata tatcattgga gcaagtgttg gatcttgtat ggaatatgga tggatcactt gtaaggacag tgcctgggaa ctggtgtagc 2940 tgcaaggatt gagaatggca tgcattagct cactttcatt taatccattg tcaaggatga 3000 3060 catgctttct tcacagtaac tcagttcaag tactatggtg atttgcctac agtgatgttt 3120 ggaatcgatc atgctttctt caaggtgaca ggtctaaaga gagaagaatc cagggaacag 3180 gtagaggaca ttgctttttc acttccaagg tgcttgatca acatctccct gacaacacaa aactagagcc aggggcctcc gtgaactccc agagcatgcc tgatagaaac tcatttctac 3240 tgttctctaa ctgtggagtg aatggaaatt ccaactgtat gttcaccctc tgaagtgggt 3300 acccagtctc ttaaatcttt tgtatttgct cacagtgttt gagcagtgct gagcacaaag 3360

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<210> 843
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<211> 805

<212> PRT

<213> homo sapiens

<400> 843

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Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp 35 40 45

Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn 50 55 60

Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala 65 70 75 80

Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln 85 90 95

Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys
100 105 110

Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser 115 120 125

Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu 130 135 140

Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu 165 170 175

Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg 180 185 190

Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
195 200 205

Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu 210 215 220

Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu 225 230 235 240

His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile 245 250 255

- Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly 265 270
- Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys 275 280 285
- Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala 290 295 300
- Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu 305 310 315 320
- Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro 325 330 335
- Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly 340 345 350
- Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp 355 360 365
- Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala 370 375 380
- Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe 385 390 395 400
- His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys 405 410 415
- His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn 420 425 430
- Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
  435 440 445
- Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe 450 455 460
- Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met 465 470 475 480
- Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr 485 490 495
- Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe 500 505 510
- Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala 515 520 525
- Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile 530 535 540
- Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu 545 550 560

- Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala 565 570 575
- Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe 580 585 590
- Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr 595 600 605
- Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu 610 615 620
- Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met 625 630 635 640
- Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu 645 650 655
- Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val 660 665 670
- Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro 675 680 685
- Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile 690 695 700
- Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn 705 710 715 720
- Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln 725 730 735
- Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val 740  $\phantom{0}$  745  $\phantom{0}$  750
- Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg 755 760 765
- Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile 770 780
- Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp 785 790 795 800
- Val Gln Thr Ser Phe
- <210> 844
- <211> 3733
- <212> DNA
- <213> homo sapiens
- <220>
- <221> misc\_feature
- <222> (40)..(40)

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<223> wherein N is either a "C" or a "T".
<220>
<221> misc_feature
<222> (47)..(47)
<223> wherein N is either an "A" or a "C".
<220>
<221> misc_feature
<222> (933)..(933)
<223> wherein N is either a "T" or a "C".
<220>
<221> misc_feature
<222> (1061)..(1061)
<223> wherein N is either a "G" or an "A".
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                                                                      60
acggcctctt tcagcgccga catgctcaat gtcaccttqc aaqqqcccac tcttaacqqq
                                                                     120
acctttgccc agagcaaatg cccccaagtg gagtggctgg gctggctcaa caccatccag
                                                                     180
coccettee tetgggtget gttegtgetg gecaecetag agaacatett tgteeteage
                                                                     240
gtettetgee tgeacaagag cagetgeacg gtggcagaga tetacetggg gaacetggee
                                                                     300
gcagcagacc tgatcctggc ctgcgggctg cccttctggg ccatcaccat ctccaacaac
                                                                     360
ttcgactggc tctttgggga gacgctctgc cgcgtggtga atqccattat ctccatqaac
                                                                     420
ctgtacagca gcatctgttt cctgatgctg gtgagcatcq accqctacct qqccctqqtq
                                                                     480
aaaaccatgt ccatgggccg gatgcgcggc gtgcgctggg ccaagctcta cagcttggtg
                                                                     540
atctgggggt gtacgctgct cctgagctca cccatgctgg tgttccggac catgaaggag
                                                                     600
tacagcgatg agggccacaa cgtcaccgct tgtgtcatca gctacccatc cctcatctqq
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gaagtgttca ccaacatgct cctgaatgtc gtgggcttcc tgctgcccct gagtgtcatc
                                                                     720
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atctgctggc tgcccttcca gatcagcacc ttcctggata cgctgcatcg cctcggcatc
                                                                     900
ctctccagct gccaggacga gcgcatcatc gangtaatca cacagatcgc ctccttcatg
                                                                     960
gcctacagca acagctgcct caacccactg gtgtacgtga tcgtgggcaa gcgcttccga
                                                                    1020
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1080

aagaagtett gggaggtgta ecagggagtg tgeeagaaag ngggetgeag gteagaacee

attcagatgg agaactccat gggcacactg cggacctcca tctccgtgga acgccagatt 1140 cacaaactgc aggactgggc agggagcaga cagtgagcaa acgccagcag ggctgctgtg 1200 aatttgtgta aggattgagg gacagttgct tttcagcatg ggcccaggaa tgccaaggag 1260 acatctatgc acgacettgg gaaatgagtt gatgteteeg gtaaaacace ggagactaat 1320 tectgeeetg cecaattttg cagggageat ggetgtgagg atggggtgaa etcacgeaca 1380 gccaaggact ccaaaatcac aacagcatta ctgttcttat ttgctgccac acctgagcca 1440 gectgeteet teeeaggagt ggaggaggee tggggggagg gagaggagtg actgagette 1500 cctcccgtgt gttctccgtc cctgccccag caagacaact tagatctcca ggagaactgc 1560 catccagctt tggtgcaatg gctgagtgca caagtgagtt gttgccctgg gtttctttaa 1620 tctattcagc tagaactttg aaggacaatt tcttgcatta ataaaggtta agccctgagg 1680 ggtccctgat aacaacctgg agaccaggat tttatggctc ccctcactga tggacaagga 1740 ggtctgtgcc aaagaagaat ccaataagca catattgagc acttgctgta tatgcagtat 1800 tgagcactgt aggcaagacc caagaaagag aaggagccat ctccatcttg aaggaactca 1860 aagactcaag tgggaacgac tgggcactgc caccaccaga aagctgttcg acgagacggt 1920 cgagcagggt gctgtgggtg atatggacag cagaaggggg agaccaaggt tccagctcaa 1980 ccaataacta ttgcacaacc acctgtccct gcctcagttc ccttttatgt aacatgaagt 2040 cgttgtgagg gttaaaggca gtaacaggta taaagtactt agaaaagcaa agggtgctac 2100 gtacatgtga ggcatcatta cgcagacgta actgggatat gtttactata aggaaaagac 2160 actgaggtct agaaatagct ccgtggagca gaatcagtat tgggagccgg tggcggtgtg 2220 aagcaccagt gtctggcaca cagtaggtgc tcattggctc ccttccacct gtcattccca 2280 ccaccctgag gccccaaccg ccacacaca aggagcattt ggagagaagg ccatgtcttc 2340 aaagtctgat ttgtgatgag gcagaggaag atatttctaa tcggtcttgc ccagaggatc 2400 acagtgctga gaccccccac caccagccgg tacctgggaa gggggagagt gcaggcctgc 2460 tragggartg ttretgtete agraaceaag ggattgttee tgtraateaa tggtttattg 2520 gaaggtggcc cagtatgagc cctagaagag tgtgaaaagg aatggcaatg gtgttcacca 2580 teggeagtge cagggeagea eteatteaet tgataaatga atatttatta getggttgga 2640 gagetagaae etggagaget agaaeetgga gaaetagaae etggaggget agaaeetgga 2700 gaggctagaa ccaagaaggg ctagaacctg gaggggctag aacctagaga agctaaaacc 2760

<221> VARIANT <222> (354)..(354)

<223> wherein Xaa is either "Gly" or a "Glu".

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                                                                     2820
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                                                                     2880
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                                                                     2940
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                                                                     3000
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                                                                     3060
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                                                                     3180
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                                                                     3240
attocctcct tacccccaac ccactctttt ttcccaccac ccactctcct ctgcctcagt
                                                                     3300
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                                                                     3360
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                                                                     3420
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gtgaaagact caatgagctg ttatgttgta aacaggaagc atttcacatc caaacgagaa
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                                                                     3720
aaaaaaaaa aaa
                                                                    3733
<210> 845
<211> 391
<212> PRT
<213> homo sapiens
<220>
<221> VARIANT
<222> (14)..(14)
<223> wherein Xaa is either "Arg" or a "Cys".
<220>
<221> VARIANT
<222> (16)..(16)
<223> wherein Xaa is either "Asp" or a "Ala".
<220>
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<400> 845

Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Xaa Glu Xaa 1 5 10 15

Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr 20 25 30

Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val 145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Ser Ser Pro Met 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val 195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr 210 215 220

Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile 225 230 235 240

Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met 245 250 255

Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val 260 265 270

Leu Val Val Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile 275 280 285

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met 305 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly 330 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln 340 345 350 Lys Xaa Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly 360 Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln 370 375 Asp Trp Ala Gly Ser Arg Gln 385 390 <210> 846 <211> 3428 <212> DNA <213> homo sapiens <400> 846 caccetatee tacactacta ggaacttgea cagteegeet egggeageee aaageteete 60 tgcccaccct ggctcccaaa accctccaaa acaaaagacc agaaaagcac tctccaccca 120 gcagccaaac gcctccttct tgacgccagc ccccaccctc tgtctgctcg agcccaggaa 180 aggcctgaag gaacaggccg gggaaggagc cctccctctc tcccttgtcc ctccatccac 240 ccagcgccgg catctggaga ccctatggcc cgggctcact ggggctgctg cccctggctg 300 gtcctcctct gtgcttgtgc ctggggccac acaaagccac tggaccttgg agggcaggat 360 gtgagaaatt gttccaccaa cccccttac cttccagtta ctgtggtcaa taccacaatg 420 teacteacag ceeteegeea geagatgeag acceagaate teteageeta cateateeca 480 ggcacagatg ctcacatgaa cgagtacatc ggccaacatg acgagaggcg tgcgtggatt 540 acaggettta cagggtetge aggaactgea gtggtgaeta tgaagaaage agetgtetgg 600 accgacagtc gctactggac tcaggctgag cggcaaatgg actgtaattg ggagctccat 660 aaggaagttg gcaccactcc tattgtcacc tggctcctca ccgagattcc tgctggaggg 720 cgtgtgggtt ttgacccctt cctcttgtcc attgacacct gggagagtta tgatctggcc 780

840

900

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<211> 673

<212> PRT

<213> homo sapiens

<400> 847

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Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val 35 40 45

Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln 50 55 60

Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu 65 70 75 80

Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr 85 90 95

Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp \$100\$ \$105 \$110

Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn Trp Glu Leu His Lys Glu Val Gly Thr Thr Pro Ile Val Thr Trp Leu Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser 420 425 430

Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu 435 440 445

Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg 450 455

Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr 465 470 475 480

Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala 485 490 495

Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp 500 505 510

Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn 515 520 525

Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile 530 540

Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys 545 550 555 560

Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu 565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe 580 585 590

Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu 595 600

His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val 610 620

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu 625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser 645 650 655

Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser 660 665 670

Val

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<211> 1082

<212> DNA

<213> homo sapiens

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<210> 849

<211> 353

<212> PRT

<213> homo sapiens

<400> 849

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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala 20 25 30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Val Phe Leu Leu

50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala 130 135 140

Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile 195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His 210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val 225 230 235 240

Gln Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val 245  $\phantom{000}250$   $\phantom{000}255$ 

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu 260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg 305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala 325 330 335

Pro Ile Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg 340 345 350

Asn

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<400> 850

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<211> 391

<212> PRT

<213> homo sapiens

<400> 851

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Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr 20 25 30

Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val 145 150 155 160

Lys	Thr	Met	Ser	Met 165	Gly	Arg	Met	Arg	Gly 170	Val	Arg	Trp	Ala	Lys 175	Leu		
Tyr	Ser	Leu	Val 180	Ile	Trp	Gly	Cys	Thr 185	Leu	Leu	Leu	Ser	Ser 190	Pro	Met		
Leu	Val	Phe 195	Arg	Thr	Met	Lys	Glu 200	Tyr	Ser	Asp	Glu	Gly 205	His	Asn	Val		
Thr	Ala 210	Cys	Val	Ile	Ser	Tyr 215	Pro	Ser	Leu	Ile	Trp 220	Glu	Val	Phe	Thr		
Asn 225	Met	Leu	Leu	Asn	Val 230	Val	Gly	Phe	Leu	Leu 235	Pro	Leu	Ser	Val	Ile 240		
Thr	Phe	Cys	Thr	Met 245	Gln	Ile	Met	Gln	Val 250	Leu	Arg	Asn	Asn	Glu 255	Met		
Gln	Lys	Phe	Lys 260	Glu	Ile	Gln	Thr	Glu 265	Arg	Arg	Ala	Thr	Val 270	Leu	Val		
Leu	Val	Val 275	Leu	Leu	Leu	Phe	Ile 280	Ile	Cys	Trp	Leu	Pro 285	Phe	Gln	Ile		
Ser	Thr 290	Phe	Leu	Asp	Thr	Leu 295	His	Arg	Leu	Gly	Ile 300	Leu	Ser	Ser	Cys		
Gln 305	Asp	Glu	Arg	Ile	Ile 310	Asp	Val	Ile	Thr	Gln 315	Ile	Ala	Ser	Phe	Met 320		
Ala	Tyr	Ser	Asn	Ser 325	Cys	Leu	Asn	Pro	Leu 330	Val	Tyr	Val	Ile	Val 335	Gly		
Lys	Arg	Phe	Arg 340	Lys	Lys	Ser	Trp	Glu 345	Val	Tyr	Gln	Gly	Val 350	Cys	Gln		
Lys	Gly	Gly 355	Cys	Arg	Ser	Glu	Pro 360	Ile	Gln	Met	Glu	Asn 365	Ser	Met	Gly		
Thr	Leu 370	Arg	Thr	Ser	Ile	Ser 375	Val	Glu	Arg	Gln	Ile 380	His	Lys	Leu	Gln		
Asp 385	Trp	Ala	Gly	Ser	Arg 390	Gln											
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gaga	cago	jtg a	aggg	etccc	c ca	ıgcct	caag	, ata	ıgccc	cctg	ccaa	ıtgct	ga d	ctttc	gaatta	1	180

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<210> 853

<211> 427

<212> PRT

<213> homo sapiens

<400> 853

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala 1 5 10 15

Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser 20 25 30

Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser 35 40 45

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr

50	55	60

Leu 65	Ile	Ala	Ser	Glu	Thr 70	Pro	Gly	Lys	Asn	Ile 75	Phe	Phe	Ser	Pro	Leu 80
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Ser	Arg	Ser	Gln 100	Ile	Leu	Glu	Gly	Leu 105	Gly	Phe	Asn	Leu	Thr 110	Glu	Leu
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Gly	Phe	Thr	Asp 340	Leu	Phe	Ser	Lys	Trp 345	Ala	Asp	Leu	Ser	Gly 350	Ile	Thr
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Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn 385 390 395 400

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    <222> (19)..(19)
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    <223> wherein "n" equals a C3 phosphoramidite linker.
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14
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               <210> 1263
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                cagcaggaaa caaataacaa gtatc
                <210> 1264
The state of the s
                <211> 27
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(II
                <213> Homo sapiens
ij
                <220>
ļ.
                <221> misc_feature
Ann And Man in the Anna in the Anna Anna Cana
                <222> (18)..(18)
                 <223> wherein "n" equals a C3 phosphoramidite linker.
                <400> 1264
ler is
                                                                                                                                                                                                                                                                                                                 27
                 acaagtatcr ggtaatgncc tctctta
                 <210> 1265
                 <211>
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                 <212> DNA
                 <213> Homo sapiens
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                 <223> wherein "n" equals a C3 phosphoramidite linker.
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                  <210> 1266
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agatctgaac atcaccgcct gcatc
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                                            wherein "n" equals a C3 phosphoramidite linker.
ļ.
Number of the State of the Stat
                 <400> 1271
                                                                                                                                                                                                                                                                                                         27
                 ttacaacata acagcncatt gagtctt
                 <210> 1272
                 <211>
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                  <213>
                                           Homo sapiens
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                  <210> 1273
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               <223> wherein "n" equals a C3 phosphoramidite linker.
               <400> 1275
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                attectteae teatntatna aacaaaa
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The state of the s
               <210> 1276
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               <400> 1276
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(II
               tacgttgagc gatgagcccc aggtt
Œ
]==½
               <210> 1277
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                <212>
                                          DNA
                <213> Homo sapiens
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                                                                                                                                                                                                                                                                                                     27
                 acaggggctg gggatngcna aatacac
                 <210> 1278
                 <211>
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   gtggtgggca cggagtcctc ac
   <210> 1279
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   <210> 1280
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   <212> DNA
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          Homo sapiens
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1,15
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ijŢ
   <222>
          (7)..(7)
I, I
   <223> wherein "n" equals a C3 phosphoramidite linker.
Ch.
₩.
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   <400> 1280
                                                                          27
   tttttgnagc cttaaaaccc ttccttc
<210> 1281
    <211> 25
    <212> DNA
    <213> Homo sapiens
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    <223> wherein "n" equals a C3 phosphoramidite linker.
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                                                                           27
    gaagtgccca ggaggctgnt gacatca
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       (15)..(15)
       wherein "n" equals a C3 phosphoramidite linker.
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gagcgaaggg ctggctgagg tcatg
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accttttgct tgatttttca ctgta
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              <220>
              <221> misc_feature
                                       (18)..(18)
              <222>
              <223> wherein "n" equals a C3 phosphoramidite linker.
              <400> 1288
                                                                                                                                                                                                                                                                                                 27
               acccacagca ccctgctnga ccgtctc
ļ.,4
               <210> 1289
A Contraction
               <211>
                                          27
               <212> DNA
               <213> Homo sapiens
ų į
<220>
(II
               <221> misc_feature
               <222>
                                        (16)..(16)
#
                                          wherein "n" equals a C3 phosphoramidite linker.
                <223>
ja i
And the control of th
                <400> 1289
                                                                                                                                                                                                                                                                                                   27
                agggttgcag ggaganctgg gatgagg
---
                <210> 1290
                <211>
                                            27
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                <220>
                 <221> misc_feature
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                                           (11)..(11)
                 <223> wherein "n" equals a C3 phosphoramidite linker.
                 <400> 1290
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                 <210> 1291
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   gttctctgga gaaaaaactg tgctg
   <210> 1292
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          wherein "n" equals a C3 phosphoramidite linker.
   <223>
   <400> 1292
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   cccctctcc aagtctntgt cccacaa
   <210> 1293
   <211> 25
   <212> DNA
Mary Mary Mary Mary Mary
   <213> Homo sapiens
   <400> 1293
                                                                           25
    gaagaggaa ctgaggcagg gacag
Ţ.
   <210> 1294
    <211> 27
3
    <212> DNA
ļ==Ē
    <213> Homo sapiens
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    <222>
          (15)..(15)
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    <223> wherein "n" equals a C3 phosphoramidite linker.
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    <210> 1295
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    <212> DNA
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    cccagcgctg gggaaagaaa ggaca
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gagatgcggt aggaagactg ttaag
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      wherein "n" equals a C3 phosphoramidite linker.
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       wherein "n" equals a C3 phosphoramidite linker.
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       Homo sapiens
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                                                                       22
aagetetace aegeettete ag
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       (10)..(10)
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<223>
<220>
 <221> misc_feature
 <222>
       (13)..(13)
 <223> wherein "n" equals a C3 phosphoramidite linker.
```

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<400> 1299
                                                                        27
   ggaacttgtn ctnctggtcc cagagca
   <210> 1300
   <211> 25
   <212> DNA
   <213> Homo sapiens
   <400> 1300
                                                                        25
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   <211> 22
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   <213> Homo sapiens
   <400> 1301
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   ccagcaggag agccaggacc ca
   <210> 1302
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   <213> Homo sapiens
   <400> 1302
                                                                         22
ccaagcgcaa ggtgagcagg gg
   <210> 1303
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                                                                         22
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    <210> 1304
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    <213> Homo sapiens
    <220>
    <221> misc_feature
          (14)..(14)
    <222>
    <223> wherein "n" equals a C3 phosphoramidite linker.
```

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<220>
   <221> misc_feature
   <222> (17)..(17)
   <223> wherein "n" equals a C3 phosphoramidite linker.
   <220>
   <221> misc_feature
          (20)..(20)
   <222>
   <223> wherein "n" equals a C3 phosphoramidite linker.
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                                                                           27
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    <210> 1305
    <211>
          27
    <212> DNA
    <213> Homo sapiens
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<221> misc_feature
    <222>
          (19)..(19)
           wherein "n" equals a C3 phosphoramidite linker.
    <223>
<400> 1305
                                                                           27
acccatactg acccttttng caagtcc
#
ļasķ
    <210> 1306
ming agen onto any
    <211> 27
    <212> DNA
    <213> Homo sapiens
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           (21)..(21)
    <222>
           wherein "n" equals a C3 phosphoramidite linker.
    <223>
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    agagcagttn gaggtcaggt ncaggga
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     <211> 25
     <212> DNA
     <213> Homo sapiens
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   <210> 1308
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   <212> DNA
   <213> Homo sapiens
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   <221> misc_feature
   <222>
          (8)..(8)
          wherein "n" equals a C3 phosphoramidite linker.
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                                                                          27
   tcccttgnac rcaggagtcc ccatccc
   <210> 1309
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ļ.
   <212> DNA
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The same
    <220>
    <221> misc_feature
1
    <222> (10)..(10)
    <223> wherein "n" equals a C3 phosphoramidite linker.
Ç.
ij
j...i
    <220>
    <221> misc_feature
<222> (14)..(14)
1.7
    <223> wherein "n" equals a C3 phosphoramidite linker.
in a
ļask
    <400> 1309
                                                                           27
    gctgtgaagn tcgnggagtt gcccacc
    <210> 1310
    <211> 22
    <212> DNA
    <213> Homo sapiens
    <400> 1310
                                                                           22
    aaggcrggga tggggactcc tg
    <210> 1311
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atgtgtgtca cgttctgcca tcacc
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      27
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      DNA
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atctggaact tatagtnttg aaaagaa
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<221> misc_feature
<222>
       (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.
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                                                                       27
gaggggttcc agangtacnt atattta
<210> 1315
<211> 25
<212> DNA
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<223> wherein "n" equals a C3 phosphoramidite linker.

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                                                                      25
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      (13)..(13)
<223> wherein "n" equals a C3 phosphoramidite linker.
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<222>
       (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.
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       (19)..(19)
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      25
<212>
       DNA
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<400> 1317
                                                                      25
gaaattttgc tgaagagaat gctaa
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<212> DNA
<213> Homo sapiens
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                                                                      25
cacatgtaaa tgactcagaa taatg
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 <211> 27
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             <213> Homo sapiens
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             <221> misc_feature
             <222>
                                      (16)..(16)
                                     wherein "n" equals a C3 phosphoramidite linker.
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             <400> 1319
                                                                                                                                                                                                                                                                             27
             ttcagttcta ggaatnatat cagacac
             <210> 1320
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              <221> misc_feature
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                                    (9)..(9)
              <223> wherein "n" equals a C3 phosphoramidite linker.
The same state of the state st
               <220>
               <221>
                                     misc_feature
               <222>
                                      (19)..(19)
IJ.
               <223> wherein "n" equals a C3 phosphoramidite linker.
Į.
as is
               <400> 1320
                                                                                                                                                                                                                                                                               27
               cttggtaana agccccatna attcttc
<210> 1321
                <211> 27
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                 <222>
                                         (15)..(15)
                                         wherein "n" equals a C3 phosphoramidite linker.
                 <223>
                 <400> 1321
                                                                                                                                                                                                                                                                                 27
                 ggntggcacc gaggntgcag cagccac
                 <210> 1322
                 <211> 27
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      wherein "n" equals a C3 phosphoramidite linker.
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       (18)..(18)
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   <223> wherein "n" equals a C3 phosphoramidite linker.
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   <221> misc_feature
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   <210> 1326
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   <212> DNA
12.0
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   <400> 1326
25
   gagggaagat tgtggatttg gtcag
ij.
ij.
<210> 1327
   <211> 25
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#
lini.
    <213> Homo sapiens
H
    <400> 1327
                                                                           25
    agaccctaaa ataaactctg aggat
jaci,
    <210> 1328
    <211>
           25
    <212>
           DNA
    <213> Homo sapiens
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           (10)..(10)
    <223> wherein "n" equals a C3 phosphoramidite linker.
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              <210> 1330
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              <400> 1330
                                                                                                                                                                                                                                                                                            39
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               <210> 1331
j., L
              <211> 39
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The state of the s
               <213> Homo sapiens
               <400> 1331
                                                                                                                                                                                                                                                                                             39
               tgtaaaacga cggccagtgg cattcacagg tgattcagt
m
              <210> 1332
               <211> 39
Ħ
               <212> DNA
jari.
               <213> Homo sapiens
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